We claim:

1. A method for identifying a candidate therapeutic agent for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component comprising:

(a) contacting a compound with a panel comprising at least one gene selected from FIGURE 1; and

(b) evaluating whether said compound is a candidate therapeutic for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component; wherein said evaluating step is performed by measuring the interaction between said compound and said gene, or by measuring a change in said gene caused by said compound.

2. The method of claim 1, wherein said compounds are selected from the following classes of compounds: antisense nucleic acids, ribozymes, siRNAs, dominant negative mutants of polypeptides encoded by the genes, small molecules, polypeptides, proteins, peptidomimetics, and nucleic acid analogs.

3. The method of claim 1, wherein said panel comprises at least one gene product selected from FIGURE 2.

4. The method of claim 1, wherein said compound is in a library of compounds.

5. The method of claim 1, wherein said library is generated using combinatorial synthetic methods.

6. The method of claim 1, wherein said evaluating step is performed using an *in vitro* assay.

7. The method of claim 1, wherein said evaluating step is performed using an *in vivo* assay.

8. A method for identifying a candidate therapeutic agent for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component comprising:

(a) contacting a compound with a panel comprising at least one gene product selected from FIGURE 1; and

(b) evaluating whether said compound is a candidate therapeutic for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component; wherein said evaluating step is performed by measuring the interaction between said compound and said gene product, or by measuring a change in said gene product caused by said compound.

9. The method of claim 8, wherein said compounds of said library are selected from the following classes of compounds: proteins, peptides, peptidomimetics, small molecules, cytokines, or hormones.

10. The method of claim 8, wherein said panel comprises at least one gene product selected from FIGURE 2.

11. The method of claim 8, wherein said compound is in a library of compounds.

12. The method of claim 8, wherein said library is generated using combinatorial synthetic methods.

13. The method of claim 8, wherein said evaluating step is performed using an *in vitro* assay.

14. The method of claim 8, wherein said evaluating step is performed using an *in vivo* assay.

15. A method for identifying a candidate therapeutic for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component, said method comprising contacting a compound with a protein encoded by the genes of FIGURE 1; wherein the ability to inhibit the protein's activity indicates a candidate therapeutic.

16. The method of claim 15, wherein said protein is encoded by the genes of FIGURE 2.

17. A method for evaluating the efficacy of a candidate therapeutic for a disorder of CD8+ T cell priming or a disease in which CD8+ T cell priming is a component, comprising treating a subject having said disorder or disease and comparing the expression levels of at least one gene in FIGURE 1 in a CD8+ T cell of said subject with that of a CD8+ T cell taken from a normal subject.

18. The method of claim 17, wherein the expression level of the genes is determined using a microarray.

19. The method of claim 17, wherein the expression level of the genes is determined using a method of RNA quantitation.

20. A solid surface to which are linked a plurality of detection agents of genes that are differentially expressed during CD8+ T cell priming, and which are capable of detecting the expression of the genes or the polypeptide encoded by the genes.

21. The solid surface of claim 20, wherein the detection agents are isolated nucleic acids which hybridize specifically to nucleic acids corresponding to the genes that are differentially expressed during CD8+ T cell priming.

22. The solid surface of claim 21, comprising isolated nucleic acids which hybridize specifically to genes in FIGURE 1.

23. The solid surface of claim 22, comprising isolated nucleic acids which hybridize specifically to genes in FIGURE 2.

24. The solid surface of claim 23, comprising isolated nucleic acids which hybridize specifically to at least 10 different nucleic acids corresponding to genes in FIGURE 1.

25. The solid surface of claim 24, comprising nucleic acids which hybridize specifically to at least 100 different nucleic acids corresponding to genes in FIGURE 1.

26. The solid surface of claim 25, comprising isolated nucleic acids which hybridize to essentially all of the to genes in FIGURE 1.

27. The solid surface of claim 20, wherein the detection agents detect the polypeptides encoded by the genes that are differentially expressed during CD8+ T cell priming.

28. The solid surface of claim 27, wherein the detection agents are antibodies reacting specifically with the polypeptides.